

FIGURE 1A

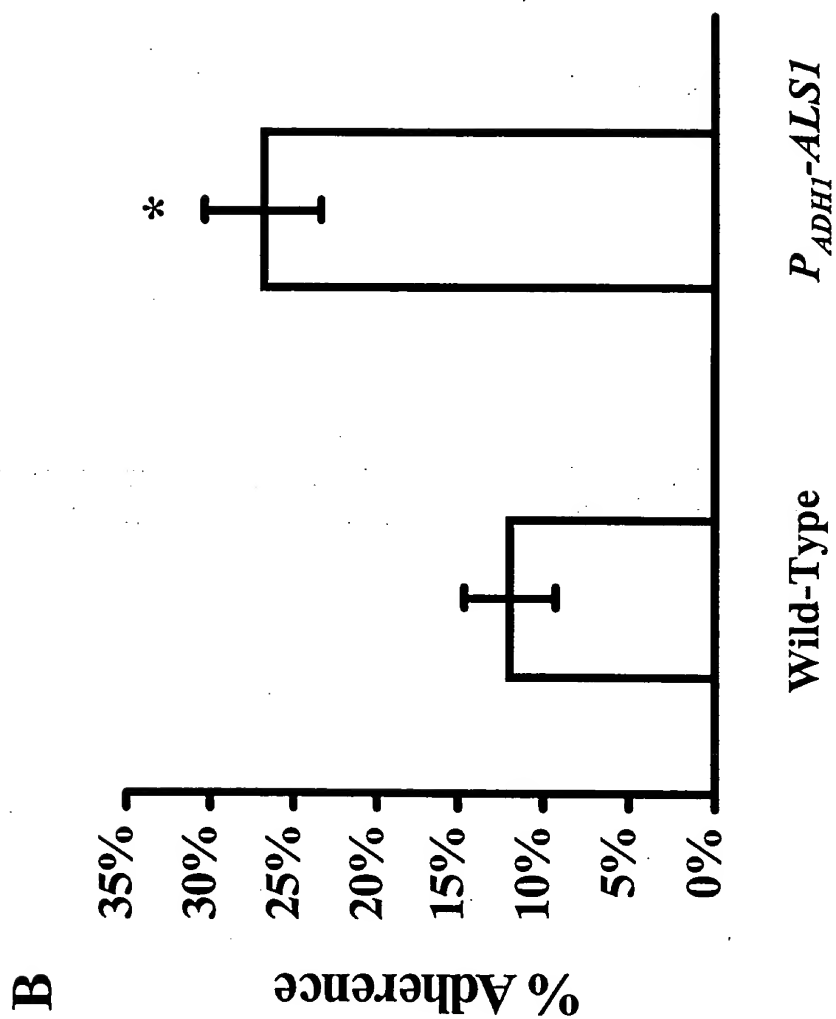


FIGURE 1B



## Wild-Type

*als1/als1*

*als1/als1::ALS1*



FIGURE 3A

[illegible]

# Wild-Type

[illegible]

[illegible]

(३)

Wild-Type

199

**Index**

CPH1/Le Jg1

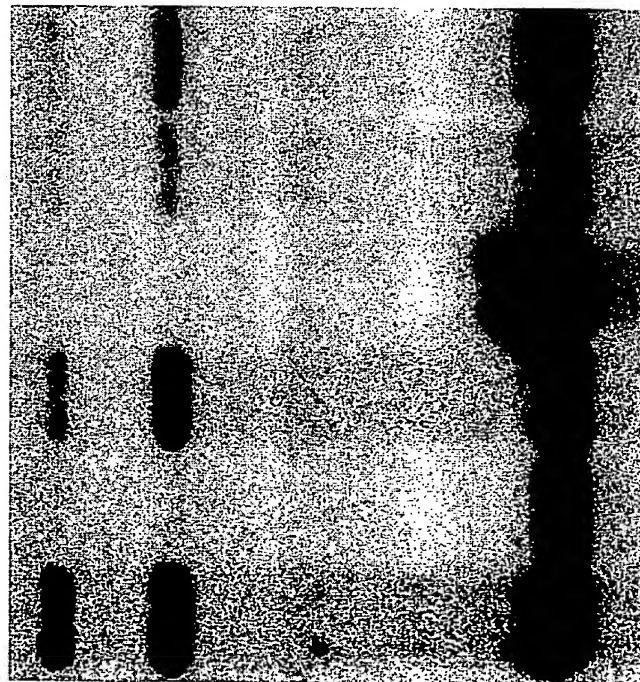
**Id m**

**Clay**

**ALSI-2**

***ALSI-1***

**ACT1**



(b)

## Wild-Type

*1891/1891*

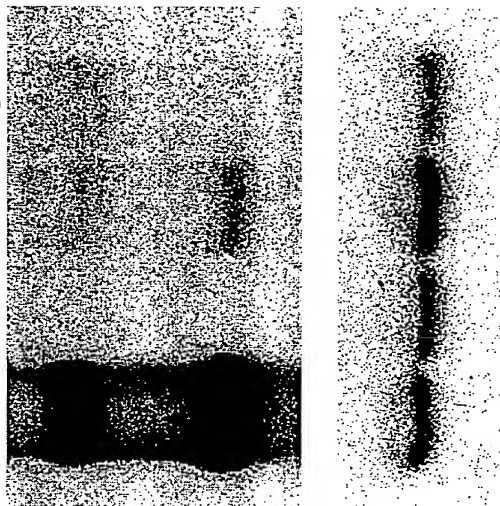
*efgi/efgi/efgi*

*efg1/efg1, P<sup>ADHI</sup>ALS1*

**TEFL**

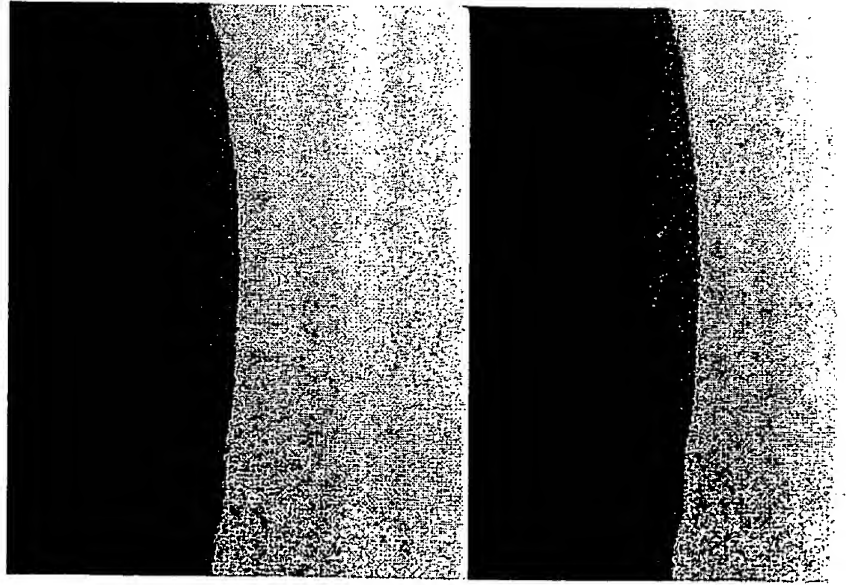
# ALSI-1

# ALSI-2



**B**

*efg1/efg1*



*efg1/efg1, P<sub>ADH1</sub> ALS1*

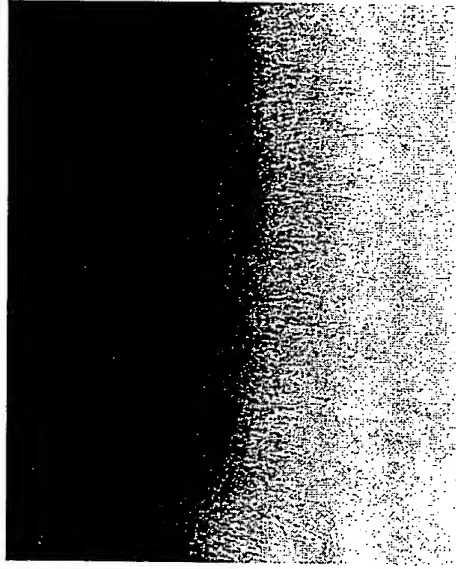


FIGURE 4B

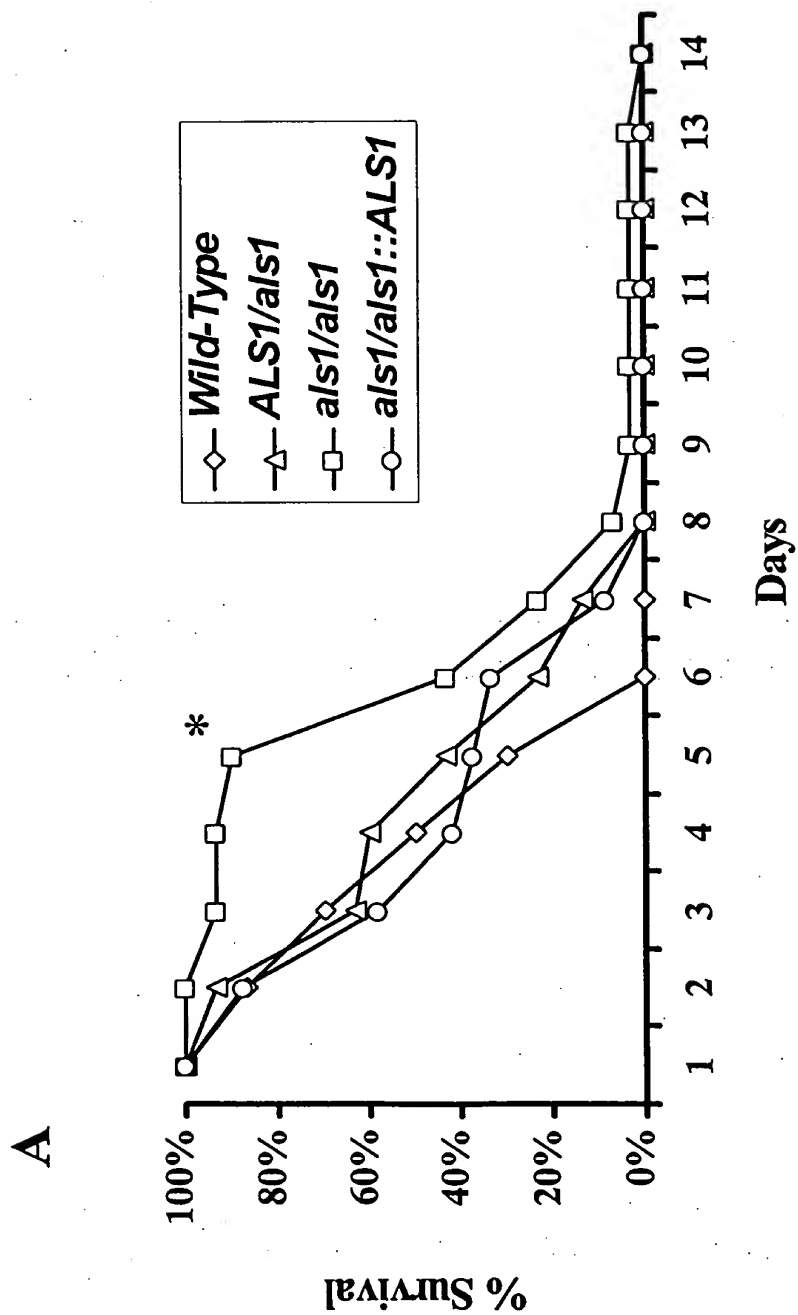


FIGURE 5A

008111-942514200

**B**

**a**

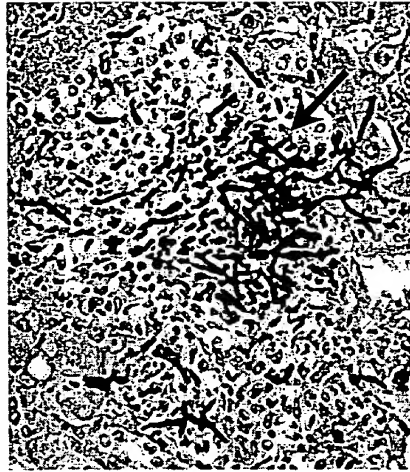
**Wild-Type**



***als1/als1***



***als1/als1::ALSI***



**b**

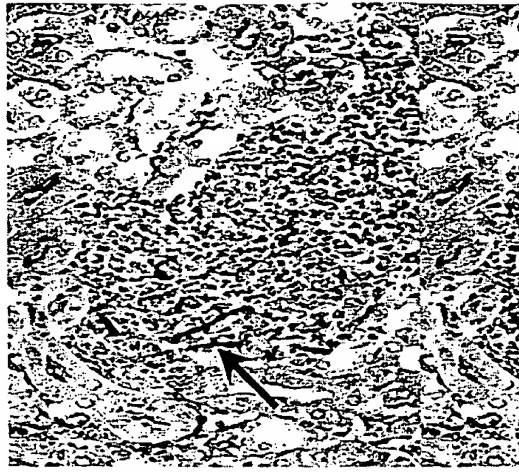
**Wild-Type**



***als1/als1***

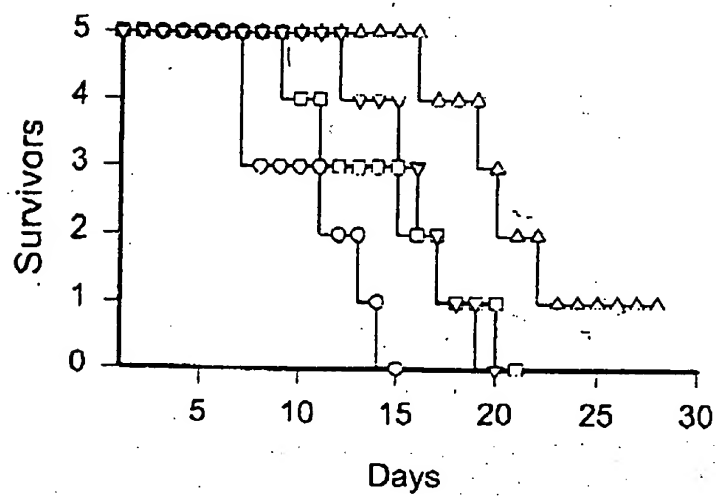


***als1/als1::ALSI***



**FIGURE 5B**

# Prophylactic effect of antiALS antibody against disseminated candidiasis



MST (days)

—○— DPBS	11.4 ± 3.3
—□— NRS (PB) <sup>1</sup>	15.4 ± 4.4
—△— S <sup>2</sup> -antiALS	22.0 ± 4.5
—▽— I <sup>3</sup> -antiALS	16.8 ± 2.6

FIGURE 6

00745875-14900

1 ATGCTTCAACAATTTACATTGTTATTCCTATATTTGTCAATTGCAAGTGCAAAGACAATC  
1 M L Q Q F T L L F L Y L S I A S A K T I  
61 ACTGGTGTTCGATAGTTTAAATTCATTAAGTGGTCCAATGCTGCTAATTATGCTTTC  
21 T G V F D S F N S L T W S N A A N Y A F  
121 AAAGGGCCAGGATACCCAACTTGAATGCTGTTTTGGGTGGTCCCTTAGATGGTACCAGT  
41 K G P G Y P T W N A V L G W S L D G T S  
181 GCCAATCCAGGGGATACATTCACATTGAATATGCCATGTGTGTTTAAATATACTACTTCA  
61 A N P G D T F T L N M P C V F K Y T T S  
241 CAAACATCTGTTGATTAACTGCCGATGGTGTAAATATGCTACTTGTCAATTTTATTCT  
81 Q T S V D L T A D G V K Y A T C Q F Y S  
301 GGTGAAGAATTCACAACTTTTCTACATTAACATGTACTGTGAACGACGCTTTGAAATCA  
101 G E E F T T F S T L T C T V N D A L K S  
361 TCCATTAAGGCATTTGGTACAGTTACTTTACCAATTGCATTCAATGTTGGTGGAAACAGGT  
121 S I K A F G T V T L P I A F N V G G T G  
421 TCATCAACTGATTGGAAGATTCTAAATGTTTTACTGCTGGTACCAATACAGTCACATTT  
141 S S T D L E D S K C F T A G T N T V T F  
481 AATGATGGTGATAAAGATATCTCAATTGATGTTGAGTTTGAAAAGTCAACCGTTGATCCA  
161 N D G D K D I S I D V E F E K S T V D P  
541 AGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCAACAACCTTTTTT  
181 S A Y L Y A S R V M P S L N K V T T L F  
601 GTGGCACCACAATGTGAAAATGGTTACACATCTGGTACAATGGGGTTCTCCAGTAGTAAC  
201 V A P Q C E N G Y T S G T M G F S S S N  
661 GGTGACGTTGCTATTGATTGCTCAAATATTCATATTGGTATCACAAAAGGATTAAATGAT  
221 G D V A I D C S N I H I G I T K G L N D  
721 TGAATTATCCGGTTTCATCTGAATCATTTAGTTACACTAAAACCTGTACATCTAATGGA  
241 W N Y P V S S E S F S Y T K T C T S N G  
781 ATTCAGATTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTTATTGATGCTTATATT  
261 I Q I K Y Q N V P A G Y R P F I D A Y I  
841 TCTGCTACAGATGTTAACCAATATACTTTAGCATATACCAATGATTATACTTGTGCTGGC  
281 S A T D V N Q Y T L A Y T N D Y T C A G  
901 AGTCGTCTGCAAAGTAAACCTTTCACTTTAAGATGGACTGGATACAAGAATAGTGATGCC  
301 S R L Q S K P F T L R W T G Y K N S D A  
961 GGATCTAACGGTATTGTCTATTGTTGCTACAACCTAGAACAGTTACAGACAGTACCCTGCT  
321 G S N G I V I V A T T R T V T D S T T A  
1021 GTCCTACTTTTACCATTCAATCCAAGTGTGATAAAACCAAAACAATCGAAATTTTGCAA

FIGURE 7

341 V T T L P F N P S V D K T K T I E I L Q  
 1081 CCTATTCCAACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCCTATCTGACT  
 361 P I P T T T I T T S Y V G V T T S Y L T  
 1141 AAGACTGCACCAATTGGTGAAACAGCTACTGTTATTGTTGATGTGCCATATCATACTACC  
 381 K T A P I G E T A T V I V D V P Y H T T  
 1201 ACAACTGTTACCAGTGAATGGACAGGAACAATCACTACCACCACAACCTCGTACCAATCCA  
 401 T T V T S E W T G T I T T T T T R T N P  
 1261 ACTGATTCAATTGACACAGTGGTGGTACAAGTTCCACTGCCAAATCCAAGTGTAGTACT  
 421 T D S I D T V V V Q V P L P N P T V S T  
 1321 ACTGAATATTGGTCTCAGTCCTTTGCTACAACCACTACAGTTACTGCTCCTCCAGGTGGT  
 441 T E Y W S Q S F A T T T T V T A P P G G  
 1381 ACCGATACTGTGATTATCAGAGAGCCACCAAACCATACTGTCACTACTACTGAATATTGG  
 461 T D T V I I R E P P N H T V T T T E Y W  
 1441 TCACAATCCTTTGCTACTACTACTACTGTTACTGCTCCTCCAGGTGGTACTGACTCAGTA  
 481 S Q S F A T T T T V T A P P G G T D S V  
 1501 ATTATCAGAGAACCACCAAATCCAAGTGTCACTACAACCGAGTATTGGTCTCAATCCTTT  
 501 I I R E P P N P T V T T T E Y W S Q S F  
 1561 GCTACTACTACTACAGTTACTGCTCCTCCAGGTGGTACTGACTCAGTAATTATCAGAGAA  
 521 A T T T T V T A P P G G T D S V I I R E  
 1621 CCTCCAAACCAACTGTCAACCACTGAATATTGGTCCCAATCTTACGCAACCACAAC  
 541 P P N P T V T T T E Y W S Q S Y A T T T  
 1681 ACTGTGACTGCTCCTCCAGGAGGCACTGACTCAGTAATTATCAGAGAACCACCAAACCAC  
 561 T V T A P P G G T D S V I I R E P P N H  
 1741 ACTGTCACTACTACTGAATACTGGTCACAATCATATGCCCACTACTCACTGTAAGTGA  
 581 T V T T T E Y W S Q S Y A T T T T V T A  
 1801 CCACCAGGTGGTACTGACACTGTTATCATTAGAGAGCCACCAAACCACACTGTCACTACT  
 601 P P G G T D T V I I R E P P N H T V T T  
 1861 ACTGAGTATTGGTCTCAATCGTTTGCTACTACCACAACCTGTAAGTGGTCCACCAAGTGGC  
 621 T E Y W S Q S F A T T T T V T G P P S G  
 1921 ACTGATACTGTTATCATTAGGGAACCACCAAACCAACTGTCACTACTACTGAATACTGG  
 641 T D T V I I R E P P N P T V T T T E Y W  
 1981 TCTCAATCATATGCAACCACTACTACCATTACCGCTCCACCTGGTGAAACTGATACCGTT  
 661 S Q S Y A T T T T I T A P P G E T D T V  
 2041 CTTATCAGAGAGCCACCAAACCATACTGTCACTACTACTGAATACTGGTCTCAATCATAT  
 681 L I R E P P N H T V T T T E Y W S Q S Y  
 2101 GCTACAACCACCACTGTTACTGCACCACCTGGTGAAACCGATACCGTTCTTATCAGAGAG  
 701 A T T T T V T A P P G E T D T V L I R E  
 2161 CCACCAAACCATACTGTCACTACTACTGAATACTGGTCTCAATCATATGCTACAACCACC

FIGURE 7

323420

721 P P N H T V T T T E Y W S Q S Y A T T T  
2221 ACTGTTACTGCACCACCAGGTGGTACCGATACTGTTATCATTAGAGAGCCACCAAATCCA  
741 T V T A P P G G T D T V I I R E P P N P  
2281 ACAGTTACTACTACTGAATATTGGTCACAATCATTTGCCACAACCACCACAGTTACTGCT  
761 T V T T T E Y W S Q S F A T T T T V T A  
2341 CCTCCAGGTGGTACTGACACTGTGATTATCTATGAAAGCATGTCAAGTTCAAAGATTTCT  
781 P P G G T D T V I I Y E S M S S S K I S  
2401 ACATCCTCCAATGATATAACCAGTATCATTCCATCATTTTCCCGTCCTCATTATGTCAAC  
801 T S S N D I T S I I P S F S R P H Y V N  
2461 AGCACAACCTCCGATTTGTCAACATTTGAATCTTCATCCATGAATACTCCTACTTCTATC  
821 S T T S D L S T F E S S S M N T P T S I  
2521 AGTAGTGATGGTATGTTGTTGTCTTCTACAACCTTTGGTTACTGAATCAGAAACAAC TACA  
841 S S D G M L L S S T T L V T E S E T T T  
2581 GAACTGATTTGCAGTGATGGTAAAGAGTGTCTAGATTGTCCAGTTCTTCTGGTATTGTC  
861 E L I C S D G K E C S R L S S S S G I V  
2641 ACAAATCCAGATAGCAATGAATCCTCAATCGTAACTAGTACTGTTTCTACTGCAAGTACA  
881 T N P D S N E S S I V T S T V P T A S T  
2701 ATGTCTGATTCACCTTTCTTCAACTGATGGTATTAGTGCTACATCTTCTGATAATGTTTCA  
901 M S D S L S S T D G I S A T S S D N V S  
2761 AAATCAGGAGTATCAGTTACAACCGAAACTTCTGTTACAAC TATTCAAAC TACTCCAAAC  
921 K S G V S V T T E T S V T T I Q T T P N  
2821 CCATTATCATCTTCAGTGACATCATTGACTCAGTTGTCTTCAATTCCAAGTGTTCAGAA  
941 P L S S S V T S L T Q L S S I P S V S E  
2881 AGTGAAAGTAAAGTTACATTTACAAGCAATGGAGACAACCAAAGTGGTACTCATGATTCA  
961 S E S K V T F T S N G D N Q S G T H D S  
2941 CAATCTACTTCCACTGAAATTGAAATTGTAACAACCAAGTTCTACTAAAGTTTACCACCT  
981 Q S T S T E I E I V T T S S T K V L P P  
3001 GTCGTTTCTTCTAATACTGATTTGACTAGTGAACCAACAAATACCAGAGAACAACCAACT  
1001 V V S S N T D L T S E P T N T R E Q P T  
3061 ACATTATCAACTACTTCAAAC TCCATCACTGAAGATATCACCACATCTCAACCTACAGGT  
1021 T L S T T S N S I T E D I T T S Q P T G  
3121 GATAATGGAGACAATACTTCATCAACCAATCCAGTTCCAAC TGTGGCAACAAGTACTTTA  
1041 D N G D N T S S T N P V P T V A T S T L  
3181 GCATCTGCAAGTGAAGAAGACAACAAAAGCGGTTCTCATGAATCAGCATCCACAAGTTTG  
1061 A S A S E E D N K S G S H E S A S T S L  
3241 AAACCAAGTATGGGTGAAAATTCTGGATTAAC TACTTCTACTGAAATTGAAGCTACAACA  
1081 K P S M G E N S G L T T S T E I E A T T  
3301 ACCAGTCCTACAGAAGCTCCATCACCTGCTGTTTCTTCTGGTACTGATGTAAC TACTGAA

FIGURE 7

1101 T S P T E A P S P A V S S G T D V T T E  
 3361 CCAACTGATACTAGAGAACAACCTACTACATTATCAACTACTTCAAAAACAAACAGTGAA  
 1121 P T D T R E Q P T T L S T T S K T N S E  
 3421 CTGGTTGCTACTACACAAGCTACTAATGAAAATGGTGGTAAATCTCCATCAACTGATTTA  
 1141 L V A T T Q A T N E N G G K S P S T D L  
 3481 ACATCAAGCTTGACAACAGGCACCTCAGCATCTACAAGTGCTAATAGCGAACTTGTTACT  
 1161 T S S L T T G T S A S T S A N S E L V T  
 3541 AGTGGATCTGTTACTGGTGGAGCTGTTGCCAGTGCTTCAAATGATCAATCACATTCTACT  
 1181 S G S V T G G A V A S A S N D Q S H S T  
 3601 TCTGTTACCAACAGCAACAGCATTGTATCTAATACCCACAAACTACATTGAGTCAACAA  
 1201 S V T N S N S I V S N T P Q T T L S Q Q  
 3661 GTTACCTCATCCTCACCTTCAACCAACACATTGCTTCTACATACGATGGCTCTGGT  
 1221 V T S S S P S T N T F I A S T Y D G S G  
 3721 TCTATTATCCAACATTCTACTTGGTTGTACGGTTTGATCACATTATTGTCCTTGTTTCATT  
 1241 S I I Q H S T W L Y G L I T L L S L F I  
 3781 TAGTGA  
 1261 \* \*

001507400

FIGURE 7